OIPE

RAW SEQUENCE LISTING   DATE: 06/13/2001
PATENT APPLICATION: US/09/836,561   TIME: 16:42:37

Input Set : N:\Crf3\RULE60\09836561.txt
Output Set: N:\CRF3\06132001\I836561.raw

ENTERED

SEQUENCE LISTING
C--> 5 (1) GENERAL INFORMATION:
      7   (i) APPLICANT: Bandman, Olga
      8   Corley, Neil C.
      9   Guegler, Karl J.
C--> 11   (ii) TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
     13   (iii) NUMBER OF SEQUENCES: 6
     15   (iv) CORRESPONDENCE ADDRESS:
     16   (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
     17   (B) STREET: 3174 Porter Drive
     18   (C) CITY: Palo Alto
     19   (D) STATE: CA
     20   (E) COUNTRY: USA
     21   (F) ZIP: 94304
     23   (v) COMPUTER READABLE FORM:
     24   (A) MEDIUM TYPE: Diskette
     25   (B) COMPUTER: IBM Compatible
     26   (C) OPERATING SYSTEM: DOS
     27   (D) SOFTWARE: FastSEQ for Windows Version 2.0
     29   (vi) CURRENT APPLICATION DATA:
C--> 30   (A) APPLICATION NUMBER: US/09/836,561
C--> 31   (B) FILING DATE: 16-Apr-2001
     32   (C) CLASSIFICATION:
     34   (vii) PRIOR APPLICATION DATA:
     35   (A) APPLICATION NUMBER: 09/212,168
     36   (B) FILING DATE:
     38   (viii) ATTORNEY/AGENT INFORMATION:
     39   (A) NAME: Billings, Lucy J.
     40   (B) REGISTRATION NUMBER: 36,749
     41   (C) REFERENCE/DOCKET NUMBER: PF-0333 US
     43   (ix) TELECOMMUNICATION INFORMATION:
     44   (A) TELEPHONE: 415-855-0555
     45   (B) TELEFAX: 415-845-4166
     46   (C) TELEX:
     49 (2) INFORMATION FOR SEQ ID NO: 1:
     51   (i) SEQUENCE CHARACTERISTICS:
     52   (A) LENGTH: 448 amino acids
     53   (B) TYPE: amino acid
     54   (C) STRANDEDNESS: single
     55   (D) TOPOLOGY: linear
     57   (vii) IMMEDIATE SOURCE:
     58   (A) LIBRARY: CORNNOT01
     59   (B) CLONE: 45517
     61   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     63 Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
     64 1   5   10   15
     65 Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp

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DATE: 06/13/2001
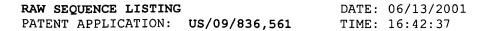TIME: 16:42:37

Input Set : **N:\Crf3\RULE60\09836561.txt**
Output Set: **N:\CRF3\06132001\I836561.raw**

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66              20                25                30
67   Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
68         35                40                45
69   Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
70      50                55                60
71   Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
72   65                70                75                80
73   Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
74                85                90                95
75   Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
76                100               105               110
77   Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
78         115               120               125
79   Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
80      130               135               140
81   Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
82   145               150               155               160
83   Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
84                165               170               175
85   Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
86                180       .       185               190
87   Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
88         195               200               205
89   Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
90      210               215               220
91   Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
92   225               230               235               240
93   Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
94                245               250               255
95   Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
96                260               265               270
97   Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
98         275               280               285
99   Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
100     290               295               300
101   Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
102  305               310               315               320
103   Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
104               325               330               335
105   Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
106               340               345               350
107   Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
108         355               360               365
109   Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
110      370               375               380
111   Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
112  385               390               395               400
113   Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
114               405               410               415
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115  Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
116          420              425              430
117  Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
118          435              440              445
120  (2) INFORMATION FOR SEQ ID NO: 2:
122      (i) SEQUENCE CHARACTERISTICS:
123          (A) LENGTH: 2550 base pairs
124          (B) TYPE: nucleic acid
125          (C) STRANDEDNESS: single
126          (D) TOPOLOGY: linear
128     (vii) IMMEDIATE SOURCE:
129          (A) LIBRARY: CORNNOT01
130          (B) CLONE: 45517
132      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
134  CCAAGATTGT TGTGAGGAGT CTAGCCAGTT GGTGAGCGCT GTAATCTGAA CCAGCTGTGT    60
135  CCAGACTGAG GCCCCATTTG CATTATTTAA CATACTTAGA AAATGAAGTG TTCATTTTTA   120
136  ACATTCCTCC TCCAATTGGT TTAATGCTGA ATTACTGAAG AGGGCTAAGC AAAACCAGGT   180
137  GCTTGCGCTG AGGGCTCTGC AGTGGCTGGG AGGACCCCGG CGCTCTCCCC GTGTCCTCTC   240
138  CACGACTCGC TCGGCCCCTC TGGAATAAAA CACCCGCGAG CCCCGAGGGC CCAGAGGAGG   300
139  CCGACGTGCC CGAGCTCCTC CGGGGGTCCC GCCCGCGAGC TTTCTTCTCG CCTTCGCATC   360
140  TCCTCCTCGC GCGTCTTGGA CATGCCAGGA ATAAAAAGGA TACTCACTGT TACCATTCTG   420
141  GCTCTCTGTC TTCCAAGCCC TGGGAATGCA CAGGCACAGT GCACGAATGG CTTTGACCTG   480
142  GATCGCCAGT CAGGACAGTG TTTAGATATT GATGAATGCC GAACCATCCC CGAGGCCTGC   540
143  CGAGGAGACA TGATGTGTGT TAACCAAAAT GGCGGGTATT TATGCATTCC CCGGACAAAC   600
144  CCTGTGTATC GAGGGCCCTA CTCGAACCCC TACTCGACCC CCTACTCAGG TCCGTACCCA   660
145  GCAGCTGCCC CACCACTCTC AGCTCCAAAC TATCCCACGA TCTCCAGGCC TCTTATATGC   720
146  CGCTTTGGAT ACCAGATGGA TGAAAGCAAC CAATGTGTGG ATGTGGACGA GTGTGCAACA   780
147  GATTCCCACC AGTGCAACCC CACCCAGATC TGCATCAATA CTGAAGGCGG GTACACCTGC   840
148  TCCTGCACCG ACGGATATTG GCTTCTGGAA GGCCAGTGCT TAGACATTGA TGAATGTCGC   900
149  TATGGTTACT GCCAGCAGCT CTGTGCGAAT GTTCCTGGAT CCTATTCTTG TACATGCAAC   960
150  CCTGGTTTTA CCCTCAATGA GGATGGAAGG TCTTGCCAAG ATGTGAACGA GTGTGCCACC  1020
151  GAGAACCCCT GCGTGCAAAC CTGCGTCAAC ACCTACGGCT CTTTCATCTG CCGCTGTGAC  1080
152  CCAGGATATG AACTTGAGGA AGATGGCGTT CATTGCAGTG ATATGGACGA GTGCAGCTTC  1140
153  TCTGAGTTCC TCTGCCAACA TGAGTGTGTG AACCAGCCCG GCACATACTT CTGCTCCTGC  1200
154  CCTCCAGGCT ACATCCTGCT GGATGACAAC CGAAGCTGCC AAGACATCAA CGAATGTGAG  1260
155  CACAGGAACC ACACGTGCAA CCTGCAGCAG ACGTGCTACA ATTTACAAGG GGGCTTCAAA  1320
156  TGCATCGACC CCATCCGCTG TGAGGAGCCT TATCTGAGGA TCAGTGATAA CCGCTGTATG  1380
157  TGTCCTGCTG AGAACCCTGG CTGCAGAGAC CAGCCCTTTA CCATCTTGTA CCGGGACATG  1440
158  GACGTGGTGT CAGGACGCTC CGTTCCCGCT GACATCTTCC AAATGCAAGC CACGACCCGC  1500
159  TACCCTGGGG CCTATTACAT TTTCCAGATC AAATCTGGGA ATGAGGGCAG AGAATTTTAC  1560
160  ATGCGGCAAA CGGGCCCCAT CAGTGCCACC CTGGTGATGA CACGCCCCAT CAAAGGGCCC  1620
161  CGGGAAATCC AGCTGGACTT GGAAATGATC ACTGTCAACA CTGTCATCAA CTTCAGAGGC  1680
162  AGCTCCGTGA TCCGACTGCG GATATATGTG TCGCAGTACC CATTCTGAGC CTCGGGCTGG  1740
163  AGCCTCCGAC GCTGCCTCTC ATTGGCACCA AGGGACAGGA GAAGAGAGGA AATAACAGAG  1800
164  AGAATGAGAG CGACACAGAC GTTAGGCATT TCCTGCTGAA CGTTTCCCCG AAGAGTCAGC  1860
165  CCCGACTTCC TGACTCTCAC CTGTACTATT GCAGACCTGT CACCCTGCAG GACTTGCCAC  1920
166  CCCCAGTTCC TATGACACAG TTATCAAAAA GTATTATCAT TGCTCCCCTG ATAGAAGATT  1980
167  GTTGGTGAAT TTTCAAGGCC TTCAGTTTAT TTCCACTATT TTCAAAGAAA ATAGATTAGG  2040
168  TTTGCGGGGG TCTGAGTCTA TGTTCAAAGA CTGTGAACAG CTTGCTGTCA CTTCTTCACC  2100
```

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Output Set: **N:\CRF3\06132001\I836561.raw**

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169  TCTTCCACTC CTTCTCTCAC TGTGTTACTG CTTTGCAAAG ACCCGGGAGC TGGCGGGGAA  2160
170  CCCTGGGAGT AGCTAGTTTG CTTTTTGCGT ACACAGAGAA GGCTATGTAA ACAAACCACA  2220
171  GCAGGATCGA AGGGTTTTTA GAGAATGTGT TTCAAAACCA TGCCTGGTAT TTTCAACCAT  2280
172  AAAAGAAGTT TCAGTTGTCC TTAAATTTGT ATAACGGTTT AATTCTGTCT TGTTCATTTT  2340
173  GAGTATTTTT AAAAAATATG TCGTAGAATT CCTTCGAAAG GCCTTCAGAC ACATGCTATG  2400
174  TTCTGTCTTC CCAAACCCAG TCTCCTCTCC ATTTTAGCCC AGTGTTTTCT TTGAGGACCC  2460
175  CTTAATCTTG CTTTCTTTAG AATTTTTACC CAATTGGATT GGAATGCAGA GGTCTCCAAA  2520
176  CTGATTAAAT ATTTGAAGAG AAAAAAAAAA                                    2550
178  (2) INFORMATION FOR SEQ ID NO: 3:
180      (i) SEQUENCE CHARACTERISTICS:
181          (A) LENGTH: 540 amino acids
182          (B) TYPE: amino acid
183          (C) STRANDEDNESS: single
184          (D) TOPOLOGY: linear
186     (vii) IMMEDIATE SOURCE:
187          (A) LIBRARY: BRAITUT13
188          (B) CLONE: 1621777
190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
192  Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
193  1               5                  10                  15
194  Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
195               20                  25                  30
196  Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
197          35                  40                  45
198  Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
199      50                  55                  60
200  His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
201  65                  70                  75                  80
202  Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
203               85                  90                  95
204  Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
205              100                 105                 110
206  Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
207              115                 120                 125
208  Gly Met Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
209          130                 135                 140
210  Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
211  145                 150                 155                 160
212  Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
213              165                 170                 175
214  Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
215              180                 185                 190
216  Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
217          195                 200                 205
218  Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
219          210                 215                 220
220  Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
221  225                 230                 235                 240
222  Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
```

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Input Set : N:\Crf3\RULE60\09836561.txt
Output Set: N:\CRF3\06132001\I836561.raw

```
223                  245              250              255
224  Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
225              260              265              270
226  Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
227          275              280              285
228  Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
229      290              295              300
230  Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
231  305              310              315              320
232  Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
233              325              330              335
234  Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
235          340              345              350
236  Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
237          355              360              365
238  Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
239      370              375              380
240  Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
241  385              390              395              400
242  Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg
243              405              410              415
244  Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
245              420              425              430
246  Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
247          435              440              445
248  Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
249      450              455              460
250  Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
251  465              470              475              480
252  Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
253              485              490              495
254  Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
255          500              505              510
256  Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
257          515              520              525
258  Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
259      530              535              540
261  (2) INFORMATION FOR SEQ ID NO: 4:
263      (i) SEQUENCE CHARACTERISTICS:
264          (A) LENGTH: 1899 base pairs
265          (B) TYPE: nucleic acid
266          (C) STRANDEDNESS: single
267          (D) TOPOLOGY: linear
269     (vii) IMMEDIATE SOURCE:
270          (A) LIBRARY: BRAITUT13
271          (B) CLONE: 162177
273      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
275  TGGGTGCAAG CTCACAACCG TAACAGCCAC CAGACAAGCT TCAGTGGCCG GCCCTTCACA      60
276  TCCAGACTTG CCTGAGAGGA CCCACCTCTG AGTGTCCAGT GGTCAGTTGC CCCAGGATGG     120
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/836,561**

DATE: 06/13/2001
TIME: 16:42:38

Input Set : **N:\Crf3\RULE60\09836561.txt**
Output Set: **N:\CRF3\06132001\I836561.raw**

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]